

# Application of molecular data to construct common bean core collection (Central and South Eastern European germplasm example)

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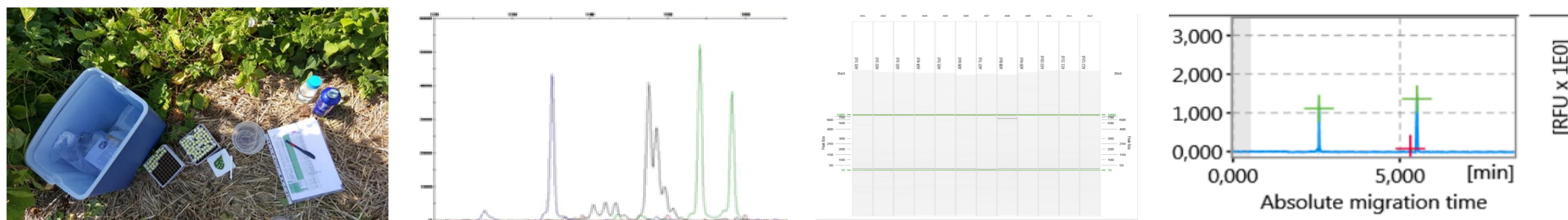
## Introduction

Genetic diversity of different genetic resources, including common bean has been evaluated in numerous studies using different DNA markers. Information on genetic diversity of common bean from Central and Eastern Europe is scarce; therefore our study was a basis for construction common bean core collection using Central and East European germplasm.



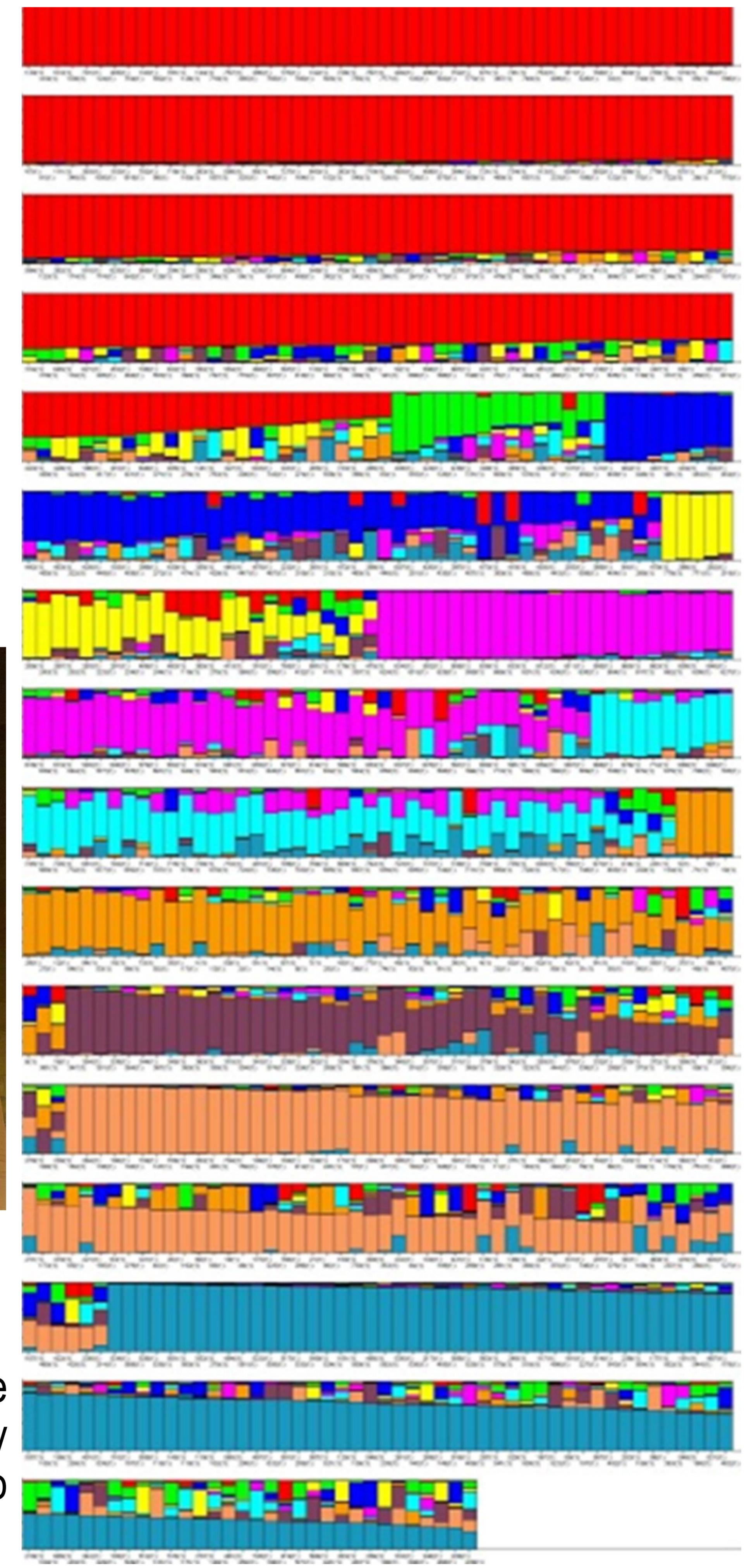
## Materials and methods

Regarding to basic multi-crop passport descriptors and seed characteristics including geographic origin, biological status, ancestral data, phenotypic seed characteristics and different phaseolin type (corresponding Andean/Mesoamerican origin), 782 accessions from **9 gene banks** and **12 geographic origins** were selected. Genotyping procedure was performed to assess their genetic background. Based on results of our recent studies and literature survey, we decided for the application of SSR markers as being informative, reliable, codominant and cost-effective. For that purpose, we selected **33 genome-specific and highly polymorphic nSSR and EST-SSR markers** with different repeat motives covering **genetic diversity of *P. vulgaris* germplasm** with equal distribution among all linkage groups among *P. vulgaris* genome (24 markers), **gene pool determination** (3 indel-spanning markers of Pv SHP1 gene) and some **trait related loci** (6 markers). Fragment analysis was performed using Genetic Analyser ABI3130XL. In total, we genotyped 25.806 electropherograms and codominant matrix of allelic profiles was obtained. Bioinformatics was performed applying different programs and software packages including GenAIEx, Structure, Structure Harvester, GenePop, Arlequin, Identity, Populations, Genetix, TreeView, MSToolkit.



## Results

Specific parameters of genetic variability showed extremely high level of genetic diversity ( $H_e=0.822$ ); cluster analysis with Bayesian approach determined real **K=10 ( $H_e > 0.65$ )**. It was also proven that selected set of nSSR and EST-SSR markers was highly informative and polymorphic (**PIC>0.8**). Obtained molecular data provided reliable information about the genetic structure, origin and genetic relations among 782 geographically and phenotypically diverse genotypes.



## Conclusion

With obtained molecular data we proposed core collection encompassing 63 highly diverse accessions covering diverse environments representing rich source of agronomically important traits and (multiple) alleles related to nutritional value and resistance potential to biotic and abiotic stress.